

SEQUENCE LISTING

<110> Ford, Gregory
Bloom, Debra
Fathman, C. Garrison

<120> Anergy Associated Genes

<130> STAN177

<140> Unassigned

<141> 2001-05-11

<150> 60/203,513

<151> 2000-05-11

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 239

<212> DNA

<213> Mus musculus

<400> 1

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agagagaagc	tgatggaaat	ttttgagtcc	cattcattag	ataattgaca	tactcagttt	180
ccttttgaac	acagtccttg	gtaataggaa	tcatacagaa	atctttttatt	tctggaaaa	239

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<211> 260

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<213> Mus musculus

<400> 2

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gatgggaagt	gtttggccat	gcttgcttgt	tggcagttaa	gacaaatgta	acacacacac	180
acacacacac	acacacacac	acacatgaga	tgagtcactg	ccttctatgg	ccttctatgg	240
tgtacgacag	ttagagatgc					260

<210> 3

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<213> Mus musculus

<400> 3

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ttacaaaccc	agcggctgcc	agttcaaaaa	atcaagacct	atatcatctg	ggagggggcc	180
atgagagctg	taatttttgt	caccaaacga	ggactaaaaa	tttgtgctga	tccagaaccc	240
aaatgggtga	aagcagcgat	caagactgtg	gatggcaggg	ccagtaccag	aaagaacatg	300
gctgaaactg	ttcccacagg	agcccagagg	tccaccagca	cagcagtaac	cctgactggg	360
taacagcctc	caggacaatg	tttccctcact	cgtaaagcag	ctcatctcag	ttcccaaacc	420

cattgcacaa atactttattt ttattttttaa cgacattcac attcattttca aatgtttataa 480
gtaataaaata tttattatttg 500

<210> 4
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<400> 4
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tttctttggg aaccatcact gttgagagggt gggggaaaac ctgaatgtaa aaagcattta 180
tttgtcaata aactgccttt tgtaaaaaaa agccctatag tgagtcgtat tacaagccga 240
ttctgcgaaa ttccatcaca ctaa 264

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<211> 2145
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (358)...(1641)

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cccgggtgga aaatcgatgg gcccgcgggc gctctagaag tactctcgag aagctttttg 180
aattcggcac gagcgcttgc ttgcaggagc tgcgtctgca gtagcctggc cgctgacgct 240
gcggtgccggc tggcagggca gcctgcgacc tcgctggccc cgcgcccgt gctagccgcc 300
ggctccccac ctggttcgca cctagtccca gcccggtcgc cctgccgagt gcgcgcc atg 360
Met
1

ggg ccg ccg ccc ggg atc ggg gtc tac tgc cgc ggc ggc tgc gga gct 408
Gly Pro Pro Pro Gly Ile Gly Val Tyr Cys Arg Gly Gly Cys Gly Ala
5 10 15

gcc cgg cta ctg gct tgg tgc ttc ctt ctg gct ctg agt ccg cac gcg 456
Ala Arg Leu Leu Ala Trp Cys Phe Leu Leu Ala Leu Ser Pro His Ala
20 25 30

ccc ggt tcc cgg gga gcc gaa gcc gtg tgg act gcg tac ctc aac gtg 504
Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn Val
35 40 45

tcc tgg cgg gtt ccg cac acc gga gtg acc gca cgg tgt gga gct gag 552
Ser Trp Arg Val Pro His Thr Gly Val Thr Ala Arg Cys Gly Ala Glu
50 55 60 65

cga gag ggc gtg tac ggc cag gac tgc ccg ctg aag ccc gtc tcc ggg 600
Arg Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Lys Pro Val Ser Gly
70 75 80

gtc ctg gta ccg ccc gac ggg ccc ggg gcg ctc aac gcc tgt aac ccg 648
Val Leu Val Pro Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn Pro
85 90 95

cac acc aat ttc acg gtg ccc acg gtt tgg ggg agc acg gtg caa gta	696
His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val Gln Val	
100 105 110	
tct tgg ttg gcc ctc atc caa cgc ggt gga ggc tgc acc ttc gcg gac	744
Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala Asp	
115 120 125	
aag atc cat ctg gct tca gag aga ggg gct tct gga gcg gtc atc ttt	792
Lys Ile His Leu Ala Ser Glu Arg Gly Ala Ser Gly Ala Val Ile Phe	
130 135 140 145	
aac ttc cct ggg acc cgc aat gag gtc atc ccc atg tct cac ccg ggt	840
Asn Phe Pro Gly Thr Arg Asn Glu Val Ile Pro Met Ser His Pro Gly	
150 155 160	
gct ggg gac att gtt gca atc atg att ggc aat ctg aaa gga aca aaa	888
Ala Gly Asp Ile Val Ala Ile Met Ile Gly Asn Leu Lys Gly Thr Lys	
165 170 175	
att ctg cag tct att caa aga ggc atc caa gtc aca atg gtc atc gaa	936
Ile Leu Gln Ser Ile Gln Arg Gly Ile Gln Val Thr Met Val Ile Glu	
180 185 190	
gta ggg aaa aaa cat ggc cct tgg gtg aat cat tat tca att ttc ttc	984
Val Gly Lys Lys His Gly Pro Trp Val Asn His Tyr Ser Ile Phe Phe	
195 200 205	
gtt tct gtg tcc ttt ttc ata att acg gca gca acc gtg ggc tat ttc	1032
Val Ser Val Ser Phe Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr Phe	
210 215 220 225	
atc ttt tat tct gct cga aga tta cga aat gca aga gct caa agc agg	1080
Ile Phe Tyr Ser Ala Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser Arg	
230 235 240	
aag cag agg cag tta aag gca gat gct aaa aaa gct att gga aag ctt	1128
Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly Lys Leu	
245 250 255	
cag ctg cgc acc ttg aaa caa gga gac aag gaa att ggc cct gat gga	1176
Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp Gly	
260 265 270	
gat agc tgt gct gtg tgc att gag ctc tat aag cca aat gat ttg gtg	1224
Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu Val	
275 280 285	
cgc atc cta acc tgc aat cat att ttc cat aag aca tgt gtg gac ccg	1272
Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val Asp Pro	
290 295 300 305	
tgg ctt tta gaa cac agg act tgc ccc atg tgc aag tgt gac att ctc	1320
Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu	
310 315 320	
aaa gct ctg gga att gag gtg gat gtt gaa gat gga tca gtg tct tta	1368
Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val Ser Leu	

325	330	335	
caa gtt cct gtt tct aat gaa gca tct aat act gcc tct ccc cat gaa			1416
Gln Val Pro Val Ser Asn Glu Ala Ser Asn Thr Ala Ser Pro His Glu			
340	345	350	
gag gac agt cgc agt gag act gca tca tct gga tat gct tca gta caa			1464
Glu Asp Ser Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val Gln			
355	360	365	
gga gca gat gag cca cct ctg gag gaa cat gcg cag tca gca aat gaa			1512
Gly Ala Asp Glu Pro Pro Leu Glu Glu His Ala Gln Ser Ala Asn Glu			
370	375	380	385
aat cta cag ctg gta aac cat gaa gca aat tct gtg gcc gtg gat gtt			1560
Asn Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val Asp Val			
390	395	400	
gtt ccc cat gtt gac aac cca acc ttt gaa gaa gat gaa act cct gat			1608
Val Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro Asp			
405	410	415	
caa gag gca gct gtt cgg gag att aaa tct taa aaatctgtgt caatagaaaa			1661
Gln Glu Ala Ala Val Arg Glu Ile Lys Ser *			
420	425		

cttgaaccgt tagttaacaa caggactgcc aatcagggcc tagtttacta tgaatgaact	1721
gggtaaacgt aaaacaagaa tgatactgaa agtgctgagg taacttatat tatactatag	1781
ttaaattggct taacatatatt accccagtac cgttttccac aaactcacca taacgttttt	1841
cataggcaag tttcctcttg gtgatagtga tagcaacatt tttaacattc agaaccgtct	1901
atgagtagtc aggttttttca tttacaacaa ctttggtata aaaaaatatg ttgctttaaa	1961
agtgtggagt agctgtaatc actttgtttt atgatagtat cataattaaa caatactact	2021
actttagctt gggctctgtg tgtcgggggt tgtctccagg tgcttatatt gatctggaat	2081
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gagc	2145

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 <211> 427
 <212> PRT
 <213> Mus musculus

<400> 6
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35 40 45
Val Ser Trp Arg Val Pro His Thr Gly Val Thr Ala Arg Cys Gly Ala
50 55 60
Glu Arg Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Lys Pro Val Ser
65 70 75 80
Gly Val Leu Val Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn
85 90 95
Pro His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val Gln
100 105 110
Val Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala
115 120 125

Asp Lys Ile His Leu Ala Ser Glu Arg Gly Ala Ser Gly Ala Val Ile
 130 135 140
 Phe Asn Phe Pro Gly Thr Arg Asn Glu Val Ile Pro Met Ser His Pro
 145 150 155 160
 Gly Ala Gly Asp Ile Val Ala Ile Met Ile Gly Asn Leu Lys Gly Thr
 165 170 175
 Lys Ile Leu Gln Ser Ile Gln Arg Gly Ile Gln Val Thr Met Val Ile
 180 185 190
 Glu Val Gly Lys Lys His Gly Pro Trp Val Asn His Tyr Ser Ile Phe
 195 200 205
 Phe Val Ser Val Ser Phe Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr
 210 215 220
 Phe Ile Phe Tyr Ser Ala Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser
 225 230 235 240
 Arg Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly Lys
 245 250 255
 Leu Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp
 260 265 270
 Gly Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu
 275 280 285
 Val Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val Asp
 290 295 300
 Pro Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile
 305 310 315 320
 Leu Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val Ser
 325 330 335
 Leu Gln Val Pro Val Ser Asn Glu Ala Ser Asn Thr Ala Ser Pro His
 340 345 350
 Glu Glu Asp Ser Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val
 355 360 365
 Gln Gly Ala Asp Glu Pro Pro Leu Glu Glu His Ala Gln Ser Ala Asn
 370 375 380
 Glu Asn Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val Asp
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 Val Val Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro
 405 410 415
 Asp Gln Glu Ala Ala Val Arg Glu Ile Lys Ser
 420 425

<210> 7
 <211> 1774
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (263)...(1547)

 <221> misc_feature
 <222> (1)...(1774)
 <223> n = A,T,C or G

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 cctggctccg acgtagctcg cagctcccca gtctcactcc attccttccc cacctggcgc 180
 gcacctgctc aagaccaggg tccctgccaa cgctaggagg gcgcgtgcc a ggggcgctag 240
 ggaactgcgg agcgcgcgcg cc atg ggg ccg ccg cct ggg gcc ggg gtc tcc 292

Met Gly Pro Pro Pro Gly Ala Gly Val Ser
1 5 10

tgc cgc ggt ggc tgc ggc ttt tcc aga ttg ctg gca tgg tgc ttc ctg	340
Cys Arg Gly Gly Cys Gly Phe Ser Arg Leu Leu Ala Trp Cys Phe Leu	
15 20 25	
ctg gcc ctg agt ccg cag gca ccc ggt tcc cgg ggg gct gaa gca gtg	388
Leu Ala Leu Ser Pro Gln Ala Pro Gly Ser Arg Gly Ala Glu Ala Val	
30 35 40	
tgg acc gcg tac ctc aac gtg tcc tgg cgg gtt ccg cac acg gga gtg	436
Trp Thr Ala Tyr Leu Asn Val Ser Trp Arg Val Pro His Thr Gly Val	
45 50 55	
aac cgt acg gtg tgg gag ctg agc gag gag ggc gtg tac ggc cag gac	484
Asn Arg Thr Val Trp Glu Leu Ser Glu Glu Gly Val Tyr Gly Gln Asp	
60 65 70	
tgc ccg ctg gag cct gtg gct ggg gtc ctg gta ccg ccc gac ggg ccc	532
Ser Pro Leu Glu Pro Val Ala Gly Val Leu Val Pro Pro Asp Gly Pro	
75 80 85 90	
ggg gcg ctt aac gcc tgt aac ccg cac acg aat ttc acg gtg ccc acg	580
Gly Ala Leu Asn Ala Cys Asn Pro His Thr Asn Phe Thr Val Pro Thr	
95 100 105	
gtt tgg gga agc acc gtg caa gtc tct tgg ttg gcc ctc atc caa cgc	628
Val Trp Gly Ser Thr Val Gln Val Ser Trp Leu Ala Leu Ile Gln Arg	
110 115 120	
ggc ggg ggc tgc acc ttc gca gac aag atc cat ctg gct tat gag aga	676
Gly Gly Gly Cys Thr Phe Ala Asp Lys Ile His Leu Ala Tyr Glu Arg	
125 130 135	
tgg gcg tct gga gcc gtc atc ttt aac ttc ccc ggg acc cgc aat gag	724
Trp Ala Ser Gly Ala Val Ile Phe Asn Phe Pro Gly Thr Arg Asn Glu	
140 145 150	
gtc atc ccc atg tct cac ccg ggt gca gta gac att gtt gca atc atg	772
Val Ile Pro Met Ser His Pro Gly Ala Val Asp Ile Val Ala Ile Met	
155 160 165 170	
atc ggc aat ctg aaa ggc aca aaa att ctg caa tct att caa aga ggc	820
Ile Gly Asn Leu Lys Gly Thr Lys Ile Leu Gln Ser Ile Gln Arg Gly	
175 180 185	
ata caa gtg aca atg gtc ata gaa gta ggg aaa aaa cat ggc cct tgg	868
Ile Gln Val Thr Met Val Ile Glu Val Gly Lys Lys His Gly Pro Trp	
190 195 200	
gtg aat cac tat tca att ttt ttc gtt tct gtg tcc ttt ttt att att	916
Val Asn His Tyr Ser Ile Phe Phe Val Ser Val Ser Phe Phe Ile Ile	
205 210 215	
acg gcg gca act gtg ggc tat ttt atc ttt tat tct gct cga agg cta	964
Thr Ala Ala Thr Val Gly Tyr Phe Ile Phe Tyr Ser Ala Arg Arg Leu	
220 225 230	

cg	g	a	a	g	c	a	a	a	a	a	c	t	a	a	g	c	a	g	a	t	1012
Arg	Asn	Ala	Arg	Ala	Gln	Ser	Arg	Lys	Gln	Arg	Gln	Leu	Lys	Ala	Asp						
235					240				245						250						
g	c	t	a	a	a	g	c	t	a	a	a	c	t	a	a	a	a	a	a	g	1060
Ala	Lys	Lys	Ala	Ile	Gly	Arg	Leu	Gln	Leu	Arg	Thr	Leu	Lys	Gln	Gly						
				255				260						265							
g	a	c	a	a	a	a	c	c	t	a	a	a	c	c	t	a	a	a	a	g	1108
Asp	Lys	Glu	Ile	Gly	Pro	Asp	Gly	Asp	Ser	Cys	Ala	Val	Cys	Ile	Glu						
			270					275					280								
t	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1156
Leu	Tyr	Lys	Pro	Asn	Asp	Leu	Val	Arg	Ile	Leu	Thr	Cys	Asn	His	Ile						
		285					290						295								
t	t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1204
Phe	His	Lys	Thr	Cys	Val	Asp	Pro	Trp	Leu	Leu	Lys	His	Lys	Thr	Cys						
	300					305					310										
c	c	c	a	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1252
Pro	Met	Cys	Lys	Cys	Asp	Ile	Leu	Lys	Ala	Leu	Gly	Ile	Glu	Val	Asp						
	315				320					325					330						
g	t	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1300
Val	Glu	Asp	Gly	Ser	Val	Ser	Leu	Gln	Val	Pro	Val	Ser	Asn	Glu	Ile						
			335					340						345							
t	c	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1348
Ser	Asn	Ser	Ala	Ser	Ser	His	Glu	Glu	Asp	Asn	Arg	Ser	Glu	Thr	Ala						
			350					355						360							
t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1396
Ser	Ser	Gly	Tyr	Ala	Ser	Val	Gln	Gly	Thr	Asp	Glu	Pro	Pro	Leu	Glu						
		365					370					375									
g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1444
Glu	His	Val	Gln	Ser	Thr	Asn	Glu	Ser	Leu	Gln	Leu	Val	Asn	His	Glu						
	380					385					390										
g	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1492
Ala	Asn	Ser	Val	Ala	Val	Asp	Val	Ile	Pro	His	Val	Asp	Asn	Pro	Thr						
	395				400					405					410						
t	t	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1540
Phe	Glu	Glu	Asp	Glu	Thr	Pro	Asn	Gln	Glu	Thr	Ala	Val	Arg	Glu	Ile						
			415					420					425								
a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1597
Lys	Ser																				
a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	g	1657
aa	ag	tg	ct	ca	ga	ta	ct	at	at	tg	ct	at	at	tg	ct	at	at	tg	ct	at	1717
tt	aa	ct	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1774

<210> 8

<211> 428
 <212> PRT
 <213> Homo sapiens

<400> 8

Met	Gly	Pro	Pro	Pro	Gly	Ala	Gly	Val	Ser	Cys	Arg	Gly	Gly	Cys	Gly	1	5	10	15
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Ala	Pro	Gly	Ser	Arg	Gly	Ala	Glu	Ala	Val	Trp	Thr	Ala	Tyr	Leu	Asn	35	40	45	
Val	Ser	Trp	Arg	Val	Pro	His	Thr	Gly	Val	Asn	Arg	Thr	Val	Trp	Glu	50	55	60	
Leu	Ser	Glu	Glu	Gly	Val	Tyr	Gly	Gln	Asp	Ser	Pro	Leu	Glu	Pro	Val	65	70	75	
Ala	Gly	Val	Leu	Val	Pro	Pro	Asp	Gly	Pro	Gly	Ala	Leu	Asn	Ala	Cys	85	90	95	
Asn	Pro	His	Thr	Asn	Phe	Thr	Val	Pro	Thr	Val	Trp	Gly	Ser	Thr	Val	100	105	110	
Gln	Val	Ser	Trp	Leu	Ala	Leu	Ile	Gln	Arg	Gly	Gly	Gly	Cys	Thr	Phe	115	120	125	
Ala	Asp	Lys	Ile	His	Leu	Ala	Tyr	Glu	Arg	Trp	Ala	Ser	Gly	Ala	Val	130	135	140	
Ile	Phe	Asn	Phe	Pro	Gly	Thr	Arg	Asn	Glu	Val	Ile	Pro	Met	Ser	His	145	150	155	
Pro	Gly	Ala	Val	Asp	Ile	Val	Ala	Ile	Met	Ile	Gly	Asn	Leu	Lys	Gly	165	170	175	
Thr	Lys	Ile	Leu	Gln	Ser	Ile	Gln	Arg	Gly	Ile	Gln	Val	Thr	Met	Val	180	185	190	
Ile	Glu	Val	Gly	Lys	Lys	His	Gly	Pro	Trp	Val	Asn	His	Tyr	Ser	Ile	195	200	205	
Phe	Phe	Val	Ser	Val	Ser	Phe	Phe	Ile	Ile	Thr	Ala	Ala	Thr	Val	Gly	210	215	220	
Tyr	Phe	Ile	Phe	Tyr	Ser	Ala	Arg	Arg	Leu	Arg	Asn	Ala	Arg	Ala	Gln	225	230	235	
Ser	Arg	Lys	Gln	Arg	Gln	Leu	Lys	Ala	Asp	Ala	Lys	Lys	Ala	Ile	Gly	245	250	255	
Arg	Leu	Gln	Leu	Arg	Thr	Leu	Lys	Gln	Gly	Asp	Lys	Glu	Ile	Gly	Pro	260	265	270	
Asp	Gly	Asp	Ser	Cys	Ala	Val	Cys	Ile	Glu	Leu	Tyr	Lys	Pro	Asn	Asp	275	280	285	
Leu	Val	Arg	Ile	Leu	Thr	Cys	Asn	His	Ile	Phe	His	Lys	Thr	Cys	Val	290	295	300	
Asp	Pro	Trp	Leu	Leu	Lys	His	Lys	Thr	Cys	Pro	Met	Cys	Lys	Cys	Asp	305	310	315	
Ile	Leu	Lys	Ala	Leu	Gly	Ile	Glu	Val	Asp	Val	Glu	Asp	Gly	Ser	Val	325	330	335	
Ser	Leu	Gln	Val	Pro	Val	Ser	Asn	Glu	Ile	Ser	Asn	Ser	Ala	Ser	Ser	340	345	350	
His	Glu	Glu	Asp	Asn	Arg	Ser	Glu	Thr	Ala	Ser	Ser	Gly	Tyr	Ala	Ser	355	360	365	
Val	Gln	Gly	Thr	Asp	Glu	Pro	Pro	Leu	Glu	Glu	His	Val	Gln	Ser	Thr	370	375	380	
Asn	Glu	Ser	Leu	Gln	Leu	Val	Asn	His	Glu	Ala	Asn	Ser	Val	Ala	Val	385	390	395	
Asp	Val	Ile	Pro	His	Val	Asp	Asn	Pro	Thr	Phe	Glu	Glu	Asp	Glu	Thr	405	410	415	
Pro	Asn	Gln	Glu	Thr	Ala	Val	Arg	Glu	Ile	Lys	Ser								

